REMARKS

Applicants believe that claims 1-3, 5-10, 27-29, 31-35, 37-46 and 55-70 are currently pending in the application. In the office action, the Examiner rejected claims 55-70. Applicants believe that claims 1-3, 5-10, 27-29, 31-35 and 37-46 are also pending in this case. Applicants respectfully request confirmation from the Examiner that claims 1-3, 5-10, 27-29, 31-35, 37-46 and 55-70 are pending.

Claims 27, 35, 44, 64 and 67 have been amended to remove the recitation of *Helianthus*. Support for these amendments is found throughout the specification, e.g., page 8, line 11 to page 9, line 12. No new matter is added by these amendments.

Rejection under 35 U.S.C. § 102

The Examiner rejected claims 55-70 under 35 U.S.C. § 102(f) because applicants did not invent the claimed subject matter. As mentioned above, applicants believe that claims 1-3, 5-10, 27-29, 31-35 and 37-46 are also pending and presume that the outstanding rejection additionally applies to these claims.

Enclosed herewith are documents to correct inventorship, including, *inter alia*, Petitions under 37 CFR § 1.48(a), petition fees, and the written consent of the assignee. Inventorship is being corrected to name Lorin R. DeBonte, Guo-Hua Miao and Zhegong Fan as the inventive entity. Upon granting of these Petitions, it is believed that the correct inventive entity is named, thereby rendering the rejection under § 102(f) moot.

Attached hereto is a marked-up version of the changes made to the claims by the current amendments. The attached page is captioned **"Version with Markings to Show Changes Made"**.

In view of the above, Applicants respectfully request reconsideration and prompt allowance of the pending claims. Please apply any other charges or credits to Deposit Account No. 06-1050.

Respectfully submitted,

Date: _____

_____
Ronald C. Lundquist, Ph.D.

Reg. No. 37,875

Fish & Richardson P.C., P.A.
60 South Sixth Street
Suite 3300
Minneapolis, MN 55402
Telephone: (612) 335-5070
Facsimile: (612) 288-9696

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the claims:

Claims 27, 35, 44, 64, and 67 have been amended as follows:

27. (Amended) An isolated nucleic acid fragment comprising a sequence of at least about 20 nucleotides from a *Brassicaceae* [or *Helianthus*] delta-15 fatty acid desaturase gene having at least one mutation in a region of said desaturase gene encoding a His-Xaa-Xaa-Xaa-His amino acid motif, wherein said at least one mutation renders the product of said desaturase gene non-functional and wherein said sequence includes said at least one mutation.

35. (Amended) A *Brassicaceae* [or *Helianthus*] plant containing a full-length coding sequence of a delta-15 fatty acid desaturase gene having at least one mutation, said at least one mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif and wherein said mutation renders the product of said desaturase gene non-functional.

44. (Amended) A *Brassicaceae* [or *Helianthus*] plant containing:

a) a full-length coding sequence from a delta-12 fatty acid desaturase gene having at least one mutation, said at least one delta-12 gene mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif; and

b) a full-length coding sequence from a delta-15 fatty acid desaturase gene having at least one mutation, said at least one delta-15 gene mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif;

wherein said delta-12 gene mutation and said delta-15 gene mutation render the products of said delta-12 desaturase gene and said delta-15 desaturase gene, respectively, non-functional.

64. (Amended) A method for producing a *Brassicaceae* [or *Helianthus*] plant line, comprising the steps of:

a) inducing mutagenesis in cells of a starting variety of a Brassicaceae or Helianthus species;

b) obtaining one or more progeny plants from said cells;

c) identifying at least one of said progeny plants that contains a delta-15 fatty acid desaturase gene having at least one mutation, said at least one mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif, wherein said at least one mutation renders the product of said delta-15 desaturase gene non-functional; and

d) producing said plant line from said at least one progeny plant by self- or cross-pollination, said plant line having said delta-15 gene mutation.

67. (Amended) A method for identifying a mutation in a *Brassicaceae* [or *Helianthus*] plant, comprising:

a) providing a *Brassicaceae* [or *Helianthus*] plant having a decreased α-linolenic acid content as compared with a corresponding control *Brassicaceae* [or *Helianthus*] plant; and

b) identifying at least one mutation in a delta-15 fatty acid desaturase gene of said plant, said at least one mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif, wherein said mutation renders the product of said delta-15 fatty acid desaturase gene non-functional.